

**AMENDMENTS TO THE CLAIMS  
PURSUANT TO WAIVER OF 37 CFR § 1.21**

1. (currently amended) A method of identifying bacteria, comprising:
  - a) providing:
    - i) amplified genomic sequences from a plurality of bacterial species arrayed on a solid support so as to create a plurality of arrayed elements, and
    - ii) labeled target DNA from a test bacteria of interest, and
    - iii) labeled reference DNA from ~~the~~ at least four strains of bacteria represented on said solid support;
  - b) hybridizing said target and reference DNA to said arrayed sequences to produce a hybridization pattern, wherein each hybridized DNA in said hybridization pattern has a signal; and
  - c) calculating the ~~ratio of each~~ hybridization signal intensity ratio at each array element to determine the identity of said test bacteria.
2. (original) The method of Claim 1, wherein said test bacteria are from a sample obtained from a subject.
3. (original) The method of Claim 1, wherein said test bacteria are pathogenic organisms.
4. (original) The method of Claim 1, wherein said test bacteria are environmental isolates.
5. (original) The method of Claim 1, wherein said solid support is a microchip.
6. (original) The method of Claim 1, wherein said calculating comprises statistical analysis.

7. (original) The method of Claim 1, wherein said signal comprises fluorescence.
8. (original) The method of Claim 1, further comprising the step of producing hybridization profiles of said test and reference bacteria.
9. (currently amended) A method of identifying bacteria, comprising:
  - a) providing:
    - i) amplified genomic sequences from a plurality of bacterial species arrayed on at least one microchip, so as to create a plurality of arrayed elements, and
    - ii) labeled target DNA from a test bacteria of interest, and
    - iii) labeled reference DNA from ~~the~~ at least four strains of bacteria represented on said at least one microchip;
  - b) hybridizing said target and reference DNA to said arrayed sequences to produce a hybridization pattern, wherein each hybridized DNA in said hybridization pattern has a signal; and;
  - c) calculating the ~~ratio of each~~ hybridization signal intensity ratio at each array element to determine the identity of said test bacteria.
10. (original) The method of Claim 9, wherein said test bacteria are from a sample obtained from a subject.
11. (original) The method of Claim 10, wherein said test bacteria are pathogenic organisms.
12. (original) The method of Claim 9, wherein said test bacteria are environmental isolates.
13. (original) The method of Claim 9, further comprising the step of producing hybridization profiles of said test and reference bacteria.

14. (original) The method of Claim 9, wherein said calculating comprises statistical analysis.
15. (original) The method of Claim 9, wherein said signal comprises fluorescence.
- 16 - 21. (currently canceled)